

FIG. 1

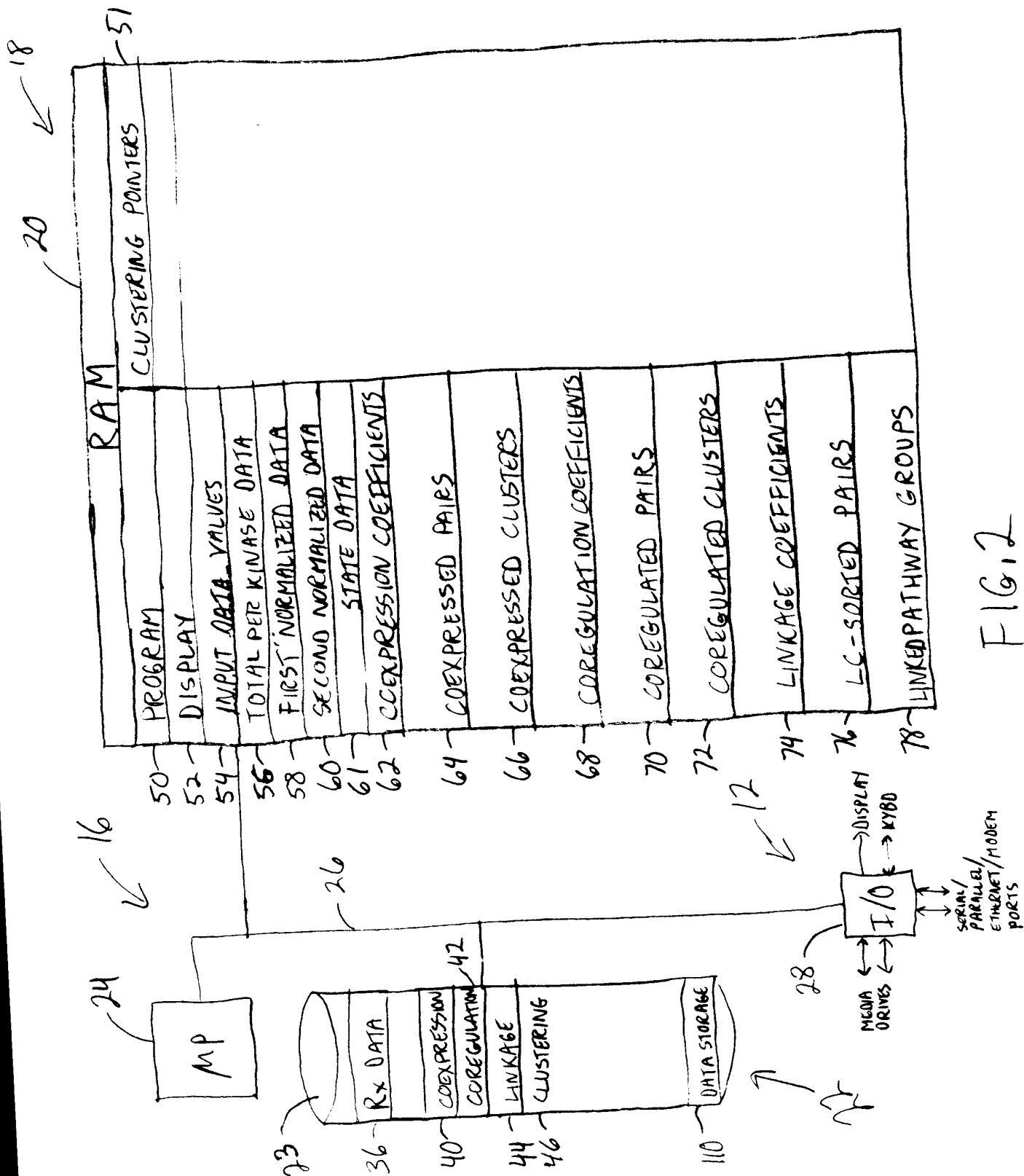


FIG. 2

RECEIVE  
ROUTINE

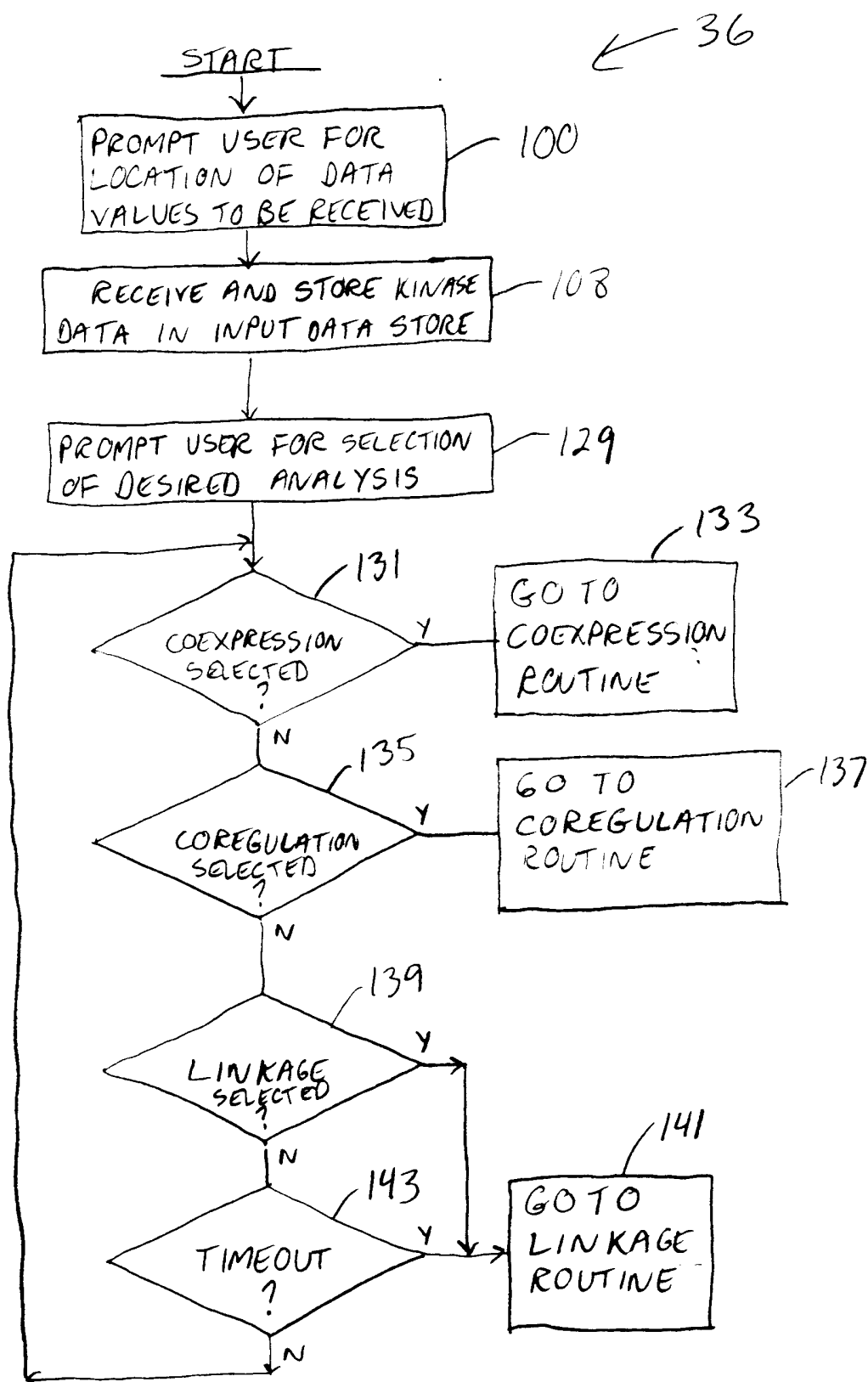


FIG. 3

# INPUT DATA VALUES STORE

54

112 { 114 120 122 124 126 202

Kinase	Phos. State	Physical Property Values in Each Model System									
		1	2	3	4	5	6	7	8	9	10
A	P	85	0	0	0	0	0	360	255	0	0
	D	0	180	142.5	160	100	95	0	0	200	90
B	P	22.5	0	0	0	0	0	85	75	0	0
	D	0	42.5	37.5	50	25	25	0	0	47.5	25
C	P	50	95	0	0	0	0	200	127.5	100	42.5
	D	0	0	63.75	100	47.5	50	0	0	0	0
D	P	190	400	0	0	0	0	800	600	300	200
	D	0	0	300	400	200	200	0	0	0	0
E	P	0	127.5	0	142.5	0	0	0	6.2	0	3.75
	D	67.5	0	112.5	0	75	75	225	6.25	0	3.75
F	P	0	50	0	50	0	0	0	0	1.3	0
	D	25	0	37.5	0	25	25	100	0	1.2	0
G	P	0	212.5	0	0	6.3	0	12.5	0	0	0
	D	112.5	0	187.5	250	6.2	0	12.5	0	0	0
H	P	0	100	0	0	0	0	14.5	0	2.5	1.2
	D	50	0	67.5	90	0	0	15.5	0	2.5	1.3
I	P	0	0	225	255	150	0	0	450	0	7.5
	D	0	0	0	0	0	150	540	0	0	7.5
J	P	0	18.75	159.4	250	125	0	0	318.8	0	0
	D	0	18.75	0	0	0	125	475	0	0	0
K	P	1.9	0	112.5	142.5	63.8	75	270	225	0	0
	D	1.85	0	0	0	0	0	0	0	0	0
L	P	0	0	75	100	45	50	200	142.5	2.6	2.4
	D	0	0	0	0	0	0	0	0	2.4	2.6
M	P	0	0	0	0	100	85	400	0	10	0
	D	0	0	0	0	0	0	0	300	10	0
N	P	2.5	2.5	0	0	25	25	100	0	0	0
	D	2.5	2.5	0	0	0	0	0	75	0	0
O	P	0	0	4.7	6.25	106.3	125	475	0	19	6.4
	D	0	0	4.7	6.25	0	0	0	318.75	18.5	6.1
P	P	0	0	0	0	150	142.5	600	0	0	0
	D	0	0	0	0	0	0	0	450	0	0
Q	P	0	0	5.625	0	0	0	0	8	100	42.5
	D	50	85	5.6	0	0	0	0	7	0	0
R	P	0	0	0	5	0	5	15	0	190	100
	D	100	200	0	5	0	5	15	0	0	0
S	P	0	0	0.95	0	1.2	0	0	0	42.5	22.5
	D	21.25	50	0.95	0	1.3	0	0	0	0	0
T	P	0	0	0	0	0	0	15	0	250	118.75
	D	125	225	0	0	0	0	15	0	0	0
Erk1	P	0	0	0	0	0	0	0	0	0	0
	D	50	100	75	100	50	50	200	150	100	50

Fig. 4

COEXPRESSION  
ROUTINE

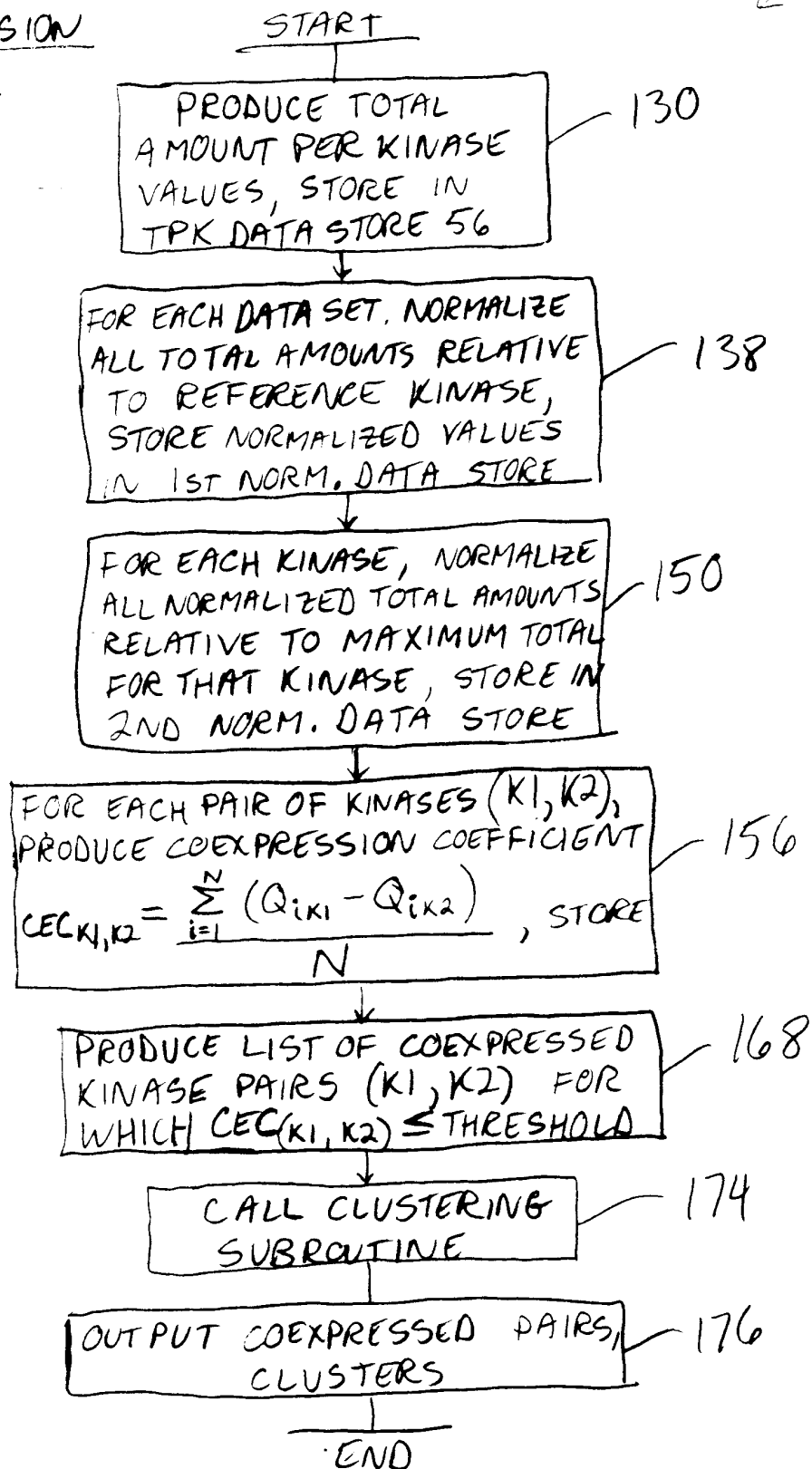


FIG. 5

# TOTAL PER PROTEIN (TPP) DATA STORE

← 56

140

134

136

System

Kinase

132 →

	1	2	3	4	5	6	7	8	9	10
A	85	180	142.5	160	100	95	360	255	200	90
B	22.5	42.5	37.5	50	25	25	85	75	47.5	25
C	50	95	63.75	100	47.5	50	200	127.5	100	42.5
D	190	400	300	400	200	200	800	600	300	200
E	67.5	127.5	112.5	142.5	75	75	255	11.25	0	7.5
F	25	50	37.5	50	25	25	100	0	2.5	0
G	112.5	212.5	187.5	250	12.5	0	25	0	0	0
H	50	100	67.5	90	0	0	30	0	5	2.5
I	0	0	225	255	150	150	540	450	0	15
J	0	37.5	159.4	250	125	125	475	318.8	0	0
K	3.75	0	112.5	142.5	63.8	75	270	225	0	0
L	0	0	75	100	45	50	200	142.5	5	5
M	0	0	0	0	100	85	400	300	20	0
N	5	5	0	0	25	25	100	75	0	0
O	0	0	9.4	12.5	106.3	125	475	318.75	37.5	12.5
P	0	0	0	0	150	142.5	600	450	0	0
Q	50	85	11.25	0	0	0	0	15	100	42.5
R	100	200	0	10	0	10	30	0	190	100
S	21.25	50	1.9	0	2.5	0	0	0	42.5	22.5
T	125	225	0	0	0	0	30	0	250	118.75
Erk1	50	100	75	100	50	50	200	150	100	50

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Erk1

142

FIG. 6

# FIRST NORMALIZED DATA

146 STORE

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System	1	2	3	4	5	6	7	8	9	10	Max
Kinase	170	180	190	160	200	190	180	170	200	180	value
A	45	42.5	50	50	50	50	42.5	50	47.5	50	200
B	100	95	85	100	95	100	100	85	100	85	50
C	380	400	400	400	400	400	400	400	300	400	100
D	135	127.5	150	142.5	150	150	127.5	7.5	0	15	400
E	50	50	50	50	50	50	50	0	2.5	0	150
F	225	212.5	250	250	25	0	12.5	0	0	0	50
G	100	100	90	90	0	0	15	0	5	5	250
H	0	0	300	255	300	300	270	300	0	30	100
I	0	37.5	212.5	250	250	250	237.5	212.5	0	0	300
J	7.5	0	150	142.5	127.5	150	135	150	0	0	250
K	0	0	100	100	90	100	100	95	5	10	150
L	0	0	0	0	200	170	200	200	20	0	100
M	10	5	0	0	50	50	50	50	0	0	200
N	0	0	12.5	12.5	212.5	250	237.5	212.5	37.5	25	50
O	0	0	0	0	300	285	300	300	0	0	250
P	0	85	15	0	0	0	0	10	100	85	300
Q	100	200	0	10	0	20	15	0	190	200	100
R	200	50	2.5	0	5	0	0	0	42.5	45	200
S	42.5	225	0	0	0	0	15	0	250	237.5	50
T	250										250

FIG. 7

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# SECOND NORMALIZED DATA STORE

System	1	2	3	4	5	6	7	8	9	10
Kinase										
154 → A	85	90	95	80	100	95	90	85	100	90
B	90	85	100	100	100	100	85	100	95	100
C	100	95	85	100	95	100	100	85	100	85
D	95	100	100	100	100	100	100	100	75	100
E	90	85	100	95	100	100	85	5	0	10
F	100	100	100	100	100	100	100	0	5	0
G	90	85	100	100	10	0	5	0	0	0
H	100	100	90	90	0	0	15	0	5	5
I	0	0	100	85	100	100	90	100	0	10
J	0	15	85	100	100	100	95	85	0	0
K	5	0	100	95	85	100	90	100	0	0
L	0	0	100	100	90	100	100	95	5	10
M	0	0	0	0	100	85	100	100	10	0
158 — [ N	10	5	0	0	100	100	100	100	0	0
O	0	0	5	5	85	100	95	85	15	10
P	0	0	0	0	100	95	100	100	0	0
Q	100	85	15	0	0	0	0	10	100	85
R	100	100	0	5	0	10	7.5	0	95	100
S	85	100	5	0	10	0	0	0	85	90
T	100	90	0	0	0	0	6	0	100	95

FIG. 8

↑ 140

← 60



# COEXPRESSION COEFFICIENTS STORE

Kinase	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
A	0	7.5	7.5	11	28.5	33	58	57.5	38	39	41.5	41	56.5	55.5	52	56.5	54.5	56.3	55.5	55.9
B	0	0	9	5.5	9.5	33	56.5	60	38	39.5	39	38.5	58.5	57	57.5	59	58	58.8	61	60.4
C	0	0	0	8.5	31	29	57.5	56	43	37.5	43	39.5	59	57	53.5	59	55	56.8	59	57.4
D	0	0	0	0	29.5	27.5	58	57.5	38.5	39	39.5	37	57	55.5	57	57.5	62.5	60.3	61.5	63.9
E	0	0	0	0	0	6.5	29	32.5	28.5	28	29.5	30	51.5	47.5	48	49.5	65.5	67.3	65.5	67.9
F	0	0	0	0	0	0	31.5	31	34	29.5	33	31.5	52	49	51.5	51	69	66.8	67	69.4
G	0	0	0	0	0	0	0	7.5	57.5	54	53	56	75.5	74.5	74	75.5	40.5	43.8	39.5	42.1
H	0	0	0	0	0	0	0	0	60	57.5	58	59.5	75.5	76	73.5	77	38	37.8	38	38.4
I	0	0	0	0	0	0	0	0	0	7.5	3	5.5	22	22	22.5	21	91	93.8	91	94.4
J	0	0	0	0	0	0	0	0	0	0	7.5	7	24.5	22.5	23	22	89.5	92.3	89.5	92.9
K	0	0	0	0	0	0	0	0	0	0	0	4.5	24.5	23	23.5	23	91	93.8	91	94.4
L	0	0	0	0	0	0	0	0	0	0	0	0	24.5	24.5	22	23.5	91.5	94.3	91.5	94.9
M	0	0	0	0	0	0	0	0	0	0	0	0	0	4	7.5	2	75	75.8	73	75.4
N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.5	2	76	76.8	74	76.4
O	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.5	71.5	72.3	69.5	72.9
P	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77	77.8	75	77.4
Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.3	8	4.6
R	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.3	3.7
S	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.6
T	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

FIG. 9 162

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166

164

172

170

$A+B, A+C, A+D$   
 $B+C, B+D, B+E$   
 $C+D$   
 $E+F$   
 $G+H$   
 $I+K, I+L, I+J$   
 $J+K, J+L$   
 $K+L$   
 $M+N, M+O, M+P$   
 $N+O, N+P$   
 $O+P$   
 $Q+R, Q+S, Q+T$   
 $R+S, R+T$   
 $S+T$

64

# COEXPRESSED PAIRS STORE

FIG. 10

# COEXPRESSED CLUSTERS STORE

- 188 →
1.  $A+B, A+C, A+D, B+C, B+D, C+D$
  2.  $J+K, J+L, K+L, I+J, I+K, I+L$
  3.  $M+N, M+O, M+P, N+O, N+P, O+P$
  4.  $Q+R, Q+S, Q+T, R+S, R+T, S+T$

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FIG. 11

CLUSTERING  
SUBROUTINE

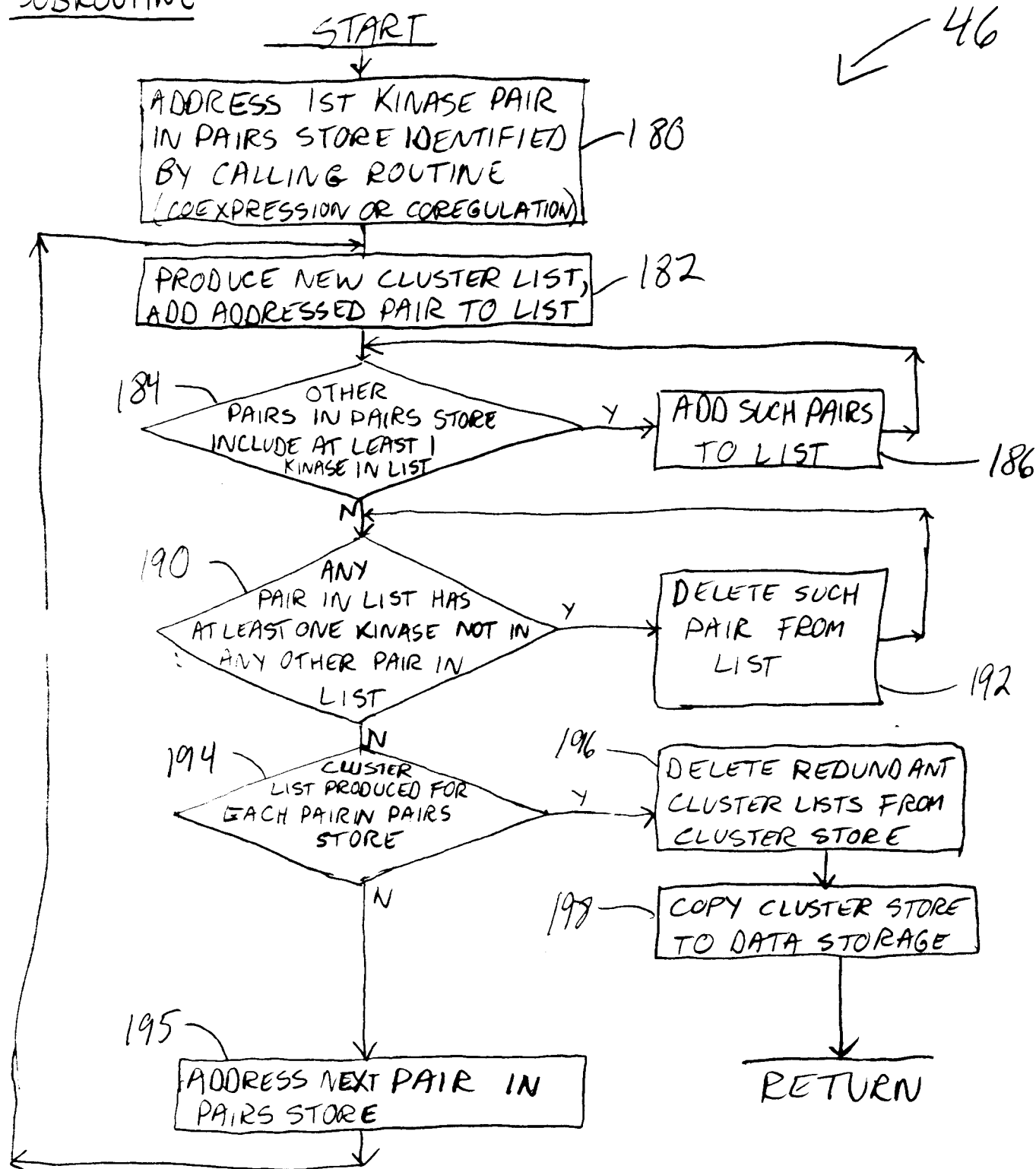


FIG. 12

# COREGULATION ROUTINE

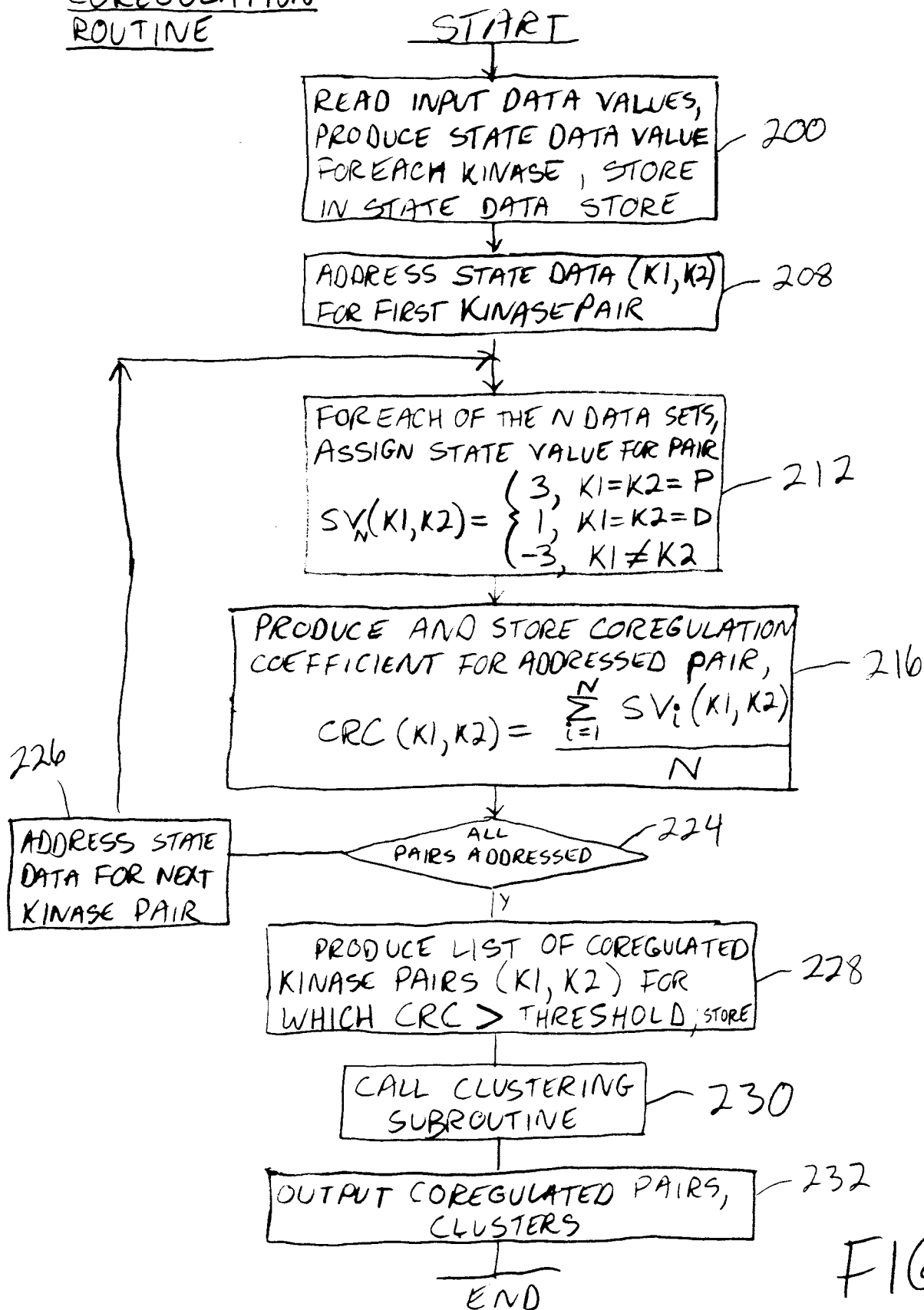


FIG.13

STATE DATA STORE

214  
↓

61  
↙

210

System  
Kinase

206 →

	1	2	3	4	5	6	7	8	9	10
A	P	D	D	D	D	D	P	P	D	D
B	P	D	D	D	D	D	P	P	D	D
C	P	P	D	D	D	D	P	P	P	P
D	P	P	D	D	D	D	P	P	P	P
E	D	P	D	D	D	D	P	P	P	P
F	D	P	D	D	D	D	P	P	P	P
G	D	P	D	D	D	D	P	P	P	P
H	D	P	D	D	D	D	P	P	P	P
I	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
J	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
K	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
L	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
M	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
N	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
O	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
P	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
Q	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
R	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
S	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.
T	N.S.	N.S.	P	P	P	D	D	P	N.S.	N.S.

FIG. 14

# COREGULATION COEFFICIENTS STORE

220 →

Kinase	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
A	0	1.6	0.4	0.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B	0	0	0.4	0.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	0	0	2.2	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0
D	0	0	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0
E	0	0	0	0	0	1.57	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0
F	0	0	0	0	0	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	0	0	0	1.5	0	0	0	0	0	0	0	0	0	0	0	0
H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0	2.33	1.0	1.0	0	0	0	0	0	0	0	0
J	0	0	0	0	0	0	0	0	0	0	1.0	1.0	0	0	0	0	0	0	0	0
K	0	0	0	0	0	0	0	0	0	0	0	3.0	1.5	1.5	1.5	1.5	0	0	0	0
L	0	0	0	0	0	0	0	0	0	0	0	0	1.5	1.5	2.5	2.5	0	0	0	0
M	0	0	0	0	0	0	0	0	0	0	0	0	0	2.5	2.5	2.5	0	0	0	0
N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
O	0	0	0	0	0	0	0	0	0	0	0	0	1.5	1.5	2.5	2.5	0	0	0	0
P	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
T	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

F16.15

↑ 222  
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### COREGULATED PAIRS

A+B, A+C, A+D

B+C, B+D

C+D, C+G, C+H

D+G, D+H

E+F, E+G, E+H

F+G, F+H

G+H

I+J, I+K, I+L

J+K, J+L

K+L, K+M, K+N, K+O, K+P

L+M, L+N, L+O, L+P

M+N, M+O, M+P

N+O, N+P

O+P

Q+R, Q+S, Q+T

R+S, R+T

S+T

← 70

FIG. 16

### COREGULATED CLUSTERS

1. A+B, A+C, A+D, B+C, B+D, C+D, C+G, C+H, D+G, D+H, E+F, E+G, E+H, F+G, F+H, G+H,

2. I+J, I+K, I+L, J+K, J+L, K+L, K+M, K+N, K+O, K+P, M+N, M+O, M+P, N+O, N+P, O+P

3. Q+R, Q+S, Q+T, R+S, R+T, S+T

FIG. 17

← 72

# LINKAGE ROUTINE

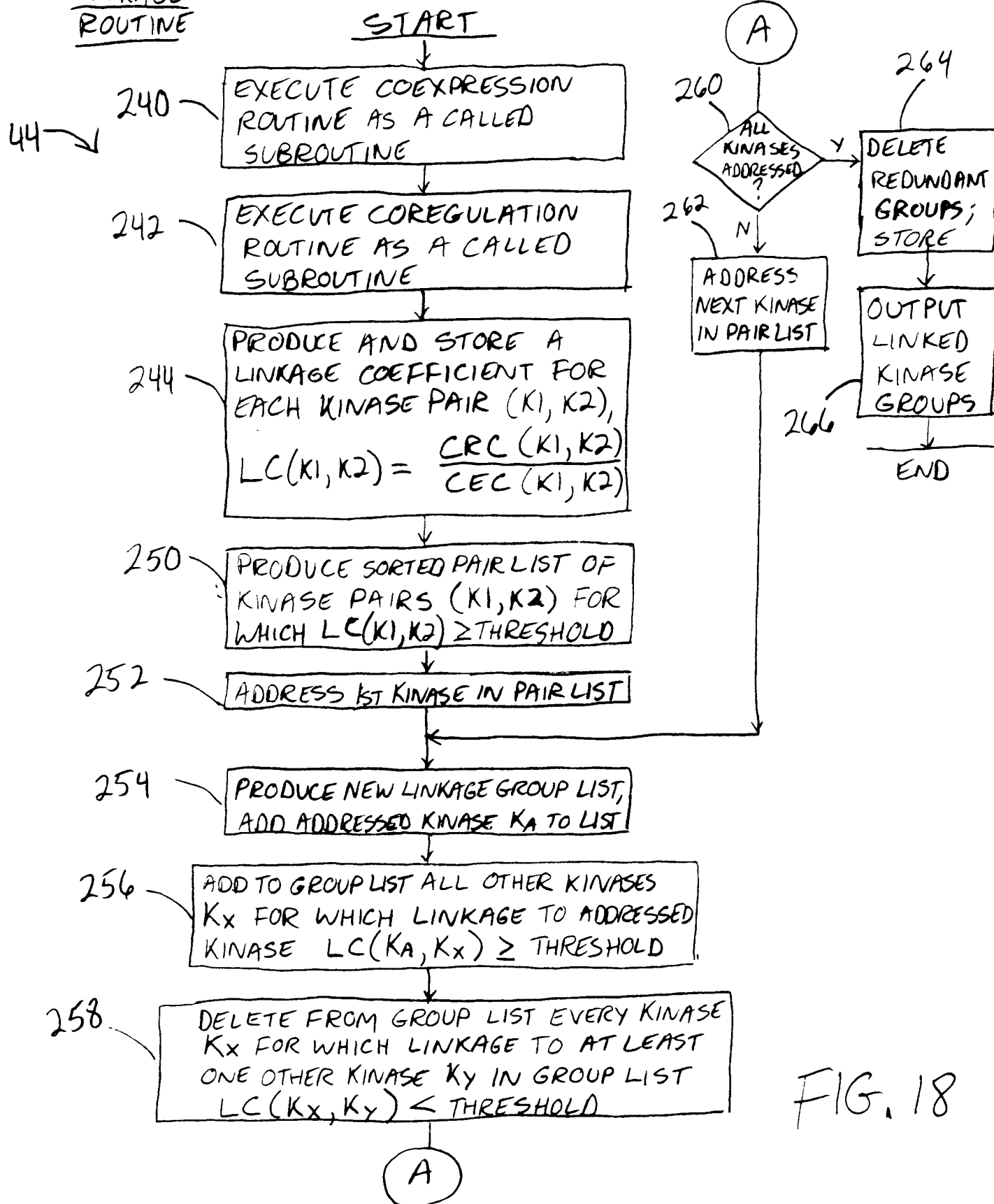


FIG. 18



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K

# LINKAGE COEFFICIENTS STORE

KinaseA		A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
248	→	0	21.3	5.3	3.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			0	4.4	7.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
				0	25.9	0	0	0.9	0.9	0	0	0	0	0	0	0	0	0	0	0	0
					0	0	0	0.9	1.7	1.5	0	0	0	0	0	0	0	0	0	0	0
						0	24.2	1.6	1.6	0	0	0	0	0	0	0	0	0	0	0	0
							0	0	20	0	0	0	0	0	0	0	0	0	0	0	0
									0	0	0	0	0	0	0	0	0	0	0	0	0
										0	31.1	33.3	18.2	0	0	0	0	0	0	0	0
											0	13.3	14.3	0	0	0	0	0	0	0	0
												0	66.7	6.1	6.5	6.4	6.5	0	0	0	0
													0	6.1	6.1	6.8	6.4	0	0	0	0
														0	62.5	33.3	125	0	0	0	0
															0	29.4	125	0	0	0	0
																0	33.3	0	0	0	0
																	0	0	0	0	0
																		0	24.1	25	43.5
																			0	27.4	54.1
																				0	30.3
																					0

FIG. 19

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↑

Pair Number	Linkage Coefficient	Kinase Pair
1	125	M, P
2	125	N, P
3	66.7	K, L
4	62.5	M, N
5	54.1	R, T
6	43.5	Q, T
7	33.3	I, K
8	33.3	M, O
9	33.3	O, P
10	31.1	I, J
11	30.3	S, T
12	29.4	N, O
13	27.4	R, S
14	25.9	C, D
15	25	Q, S
16	24.2	E, F
17	24.1	Q, R
18	21.3	A, B
19	20	G, H
20	18.2	I, L
21	14.3	J, L
22	13.3	J, K
23	7.3	B, D
24	6.8	L, O
25	6.5	K, N
26	6.5	K, P
27	6.4	K, O
28	6.4	L, P
29	6.1	K, M
30	6.1	L, M
31	6.1	L, N
32	5.3	A, C
33	4.4	B, C
34	3.6	A, D
35	1.7	E, G
36	1.6	F, G
37	1.6	F, H
38	1.5	E, H
39	0.9	C, G
40	0.9	C, H
41	0.9	D, G
42	0.9	D, H

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**Fig. 20**

1. A, B, C, D
- 257 → 2. C, D, G, H
3. E, F, G, H
4. I, J, K, L
5. K, L, M, N, O, P
6. Q, R, S, T

Fig. 21